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 |_|        |_| |_|  |___| |_| \_\ |___| |_| |_|   (TM)

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            Release 2.1D John F. Collins, Biocomputing Research Unit.
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 MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

 Run on: Tue Jan 21 20:00:57 1997; MasPar time 258.17 Seconds
                                                898.654 Million cell updates/sec
 Tabular output not generated.

 Title: >US-08-469-637-1
 Description: (1-1173) from US08469637.seq
 Perfect Score: 1173
 N.A. Sequence: 1 ATGAACAAGTTGCTGTGCTG..........TTTTTAGAAATGATAGGTAA 1173
         Comp: TACTTGTTCAACGACACGAC..........AAAAATCTTTACTATCCATT

 Scoring table: TABLE default
                    Gap 6

 Nmatch   STD :   Dbase 0; Query 0

 Searched: 283905 seqs, 98892167 bases x 2

 Post-processing: Minimum Match 0%
                    Listing first 45 summaries

 Database: EST-STS-TWO
                    1:EST100 2:EST101 3:EST102 4:EST103 5:EST104 6:EST105
                    7:EST106 8:EST107 9:EST108 10:EST109 11:EST110 12:EST111
                    13:EST112 14:EST113 15:EST114 16:EST115 17:EST116
                    18:EST117 19:EST118 20:EST119 21:EST120 22:EST121
                    23:EST122 24:EST123 25:EST124 26:EST125 27:EST126
                    28:EST127 29:EST128 30:STS1 31:STS2 32:STS3 33:STS4
                    34:STS5 35:STS6 36:STS7 37:STS8 38:STS9 39:STS10
                    40:ueEST 41:gnEST1 42:gnEST2 43:gnEST3 44:gnEST4
                    45:gnEST5 46:gnEST6 47:gnEST7 48:gnEST8 49:gnEST9
                    50:gnEST10 51:gnEST11 52:gnEST12 53:gnEST13 54:gnEST14
                    55:gnEST15 56:gnEST16 57:gnSTS 58:enEST1 59:enEST2
                    60:enEST3 61:enEST4 62:enEST5 63:enEST6 64:enEST7
                    65:enEST8 66:enEST9 67:enEST10 68:enEST11 69:enEST12
                    70:enEST13 71:enEST14 72:enEST15 73:enEST16 74:enSTS1
                    75:enSTS2

Statistics: Mean 11.091; Variance 1.948; scale 5.692

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
c	1	23	2.0	442	21	T71938	ye07c04.r1 Homo sapie	9.30e-06
c	2	24	2.0	504	21	T72414	yc72a07.r1 Homo sapie	4.26e-07
c	3	22	1.9	267	71	MM5835	ma38f10.r1 Soares mou	1.81e-04
c	4	22	1.9	267	50	W10583	ma38f10.r1 Soares mou	1.81e-04
c	5	22	1.9	330	2	RICC0437A	Rice cDNA, partial se	1.81e-04
c	6	22	1.9	400	33	G10922	human STS SHGC-13782	1.81e-04
	7	22	1.9	410	22	T74804	yc60d04.r1 Homo sapie	1.81e-04
	8	22	1.9	450	39	HUMUT1054	Human STS UT1054.	1.81e-04
c	9	22	1.9	465	23	T77351	yd72e10.r1 Homo sapie	1.81e-04
	10	22	1.9	472	14	T42477	5740 Arabidopsis thal	1.81e-04
	11	22	1.9	493	3	RICS15559A	Rice cDNA, partial se	1.81e-04
	12	21	1.8	105	70	MM1135	ma42d03.r1 Soares mou	3.12e-03
	13	21	1.8	105	50	W10113	ma42d03.r1 Soares mou	3.12e-03
	14	21	1.8	194	39	HUMUT5145	Human STS UT5145.	3.12e-03
c	15	21	1.8	245	34	G11923	human STS MR4116.	3.12e-03
	16	21	1.8	253	32	G06067	human STS WI-6406.	3.12e-03
c	17	21	1.8	325	17	T54964	yb42d03.r1 Homo sapie	3.12e-03
	18	21	1.8	351	57	DM122E4S	D. melanogaster STS d	3.12e-03
	19	21	1.8	351	30	DM122E4S	D. melanogaster STS d	3.12e-03
	20	21	1.8	351	74	DM122E4S	D. melanogaster STS d	3.12e-03
c	21	21	1.8	362	21	T70903	yc49d03.s1 Homo sapie	3.12e-03
c	22	21	1.8	371	73	TG1651	TgESTzy27b03.r1 Toxop	3.12e-03
c	23	21	1.8	371	41	N61165	TgESTzy27b03.r1 Toxop	3.12e-03
	24	21	1.8	376	65	HS639308	yv67g05.r1 Homo sapie	3.12e-03
	25	21	1.8	376	42	N77639	yv67g05.r1 Homo sapie	3.12e-03
c	26	21	1.8	376	21	T71088	yc50d04.r1 Homo sapie	3.12e-03
	27	21	1.8	377	70	MM05110	mb83g02.r1 Soares mou	3.12e-03
	28	21	1.8	377	52	W18051	mb83g02.r1 Soares mou	3.12e-03
	29	21	1.8	386	37	HSA132ZC9	H. sapiens (D2S400) D	3.12e-03
	30	21	1.8	392	5	T03759	IB862 Homo sapiens cD	3.12e-03
c	31	21	1.8	395	21	T71079	yc50c04.r1 Homo sapie	3.12e-03
	32	21	1.8	450	73	TG8862	TgESTzy39d10.r1 Toxop	3.12e-03
	33	21	1.8	450	41	N68886	TgESTzy39d10.r1 Toxop	3.12e-03
c	34	21	1.8	496	46	N96353	21953 Arabidopsis tha	3.12e-03
c	35	21	1.8	496	58	AT35319	21953 Arabidopsis tha	3.12e-03
c	36	21	1.8	1035	53	W18541	mb68f10.r1 Soares mou	3.12e-03
c	37	21	1.8	1035	71	MM54110	mb68f10.r1 Soares mou	3.12e-03
	38	20	1.7	271	21	T69650	yc44c09.r1 Homo sapie	4.71e-02
c	39	20	1.7	408	22	T74544	yc56a04.s1 Homo sapie	4.71e-02
c	40	20	1.7	411	15	T48207	yb44a06.s1 Homo sapie	4.71e-02
c	41	20	1.7	416	21	T69287	yc37f07.s1 Homo sapie	4.71e-02
c	42	20	1.7	509	18	T61115	yc45f06.s1 Homo sapie	4.71e-02
	43	20	1.7	510	46	N96182	21638 Arabidopsis tha	4.71e-02

```
c   44      20      1.7     526 20  T68555      yc43b05.s1 Homo sapie  4.71e-02
    45      20      1.7     572 65  HS673328    zb36a06.r1 Soares par  4.71e-02
```

ALIGNMENTS

```
RESULT    1
LOCUS       T71938        442 bp      mRNA            EST        16-MAR-1995
DEFINITION  ye07c04.r1 Homo sapiens cDNA clone 117030 5' similar to
            gb:X54486_rna1 PLASMA PROTEASE C1 INHIBITOR PRECURSOR (HUMAN);.
ACCESSION   T71938
NID         g686459
KEYWORDS    EST.
SOURCE      human clone=117030 library=Stratagene lung (#937210)
            vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
            primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72
            year old male. Cloned unidirectionally. Primer: Oligo dT. Average
            insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
            5'-GAATTCGGCACGAG-3'; 3' adaptor sequence:
            5'-CTCGAGTTTTTTTTTTTTTTTTTT-3'.
  ORGANISM  Homo sapiens
            Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
            Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High qality sequence stops: 265
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
     source          1..442
                     /organism="Homo sapiens"
                     /clone="117030"
                     /note="human"
BASE COUNT      120 a     117 c      96 g      108 t       1 others
ORIGIN

     Query Match              2.0%;   Score 23;  DB 21;  Length 442;
     Best Local Similarity 79.5%;   Pred. No. 9.30e-06;
     Matches    31; Conservative    0; Mismatches   8; Indels   0; Gaps   0;
```

```
Db    332 aggacatgggaacagggttttcaggcctttcttgttttt 370
          ||||  |||  || |||||| || ||||||| ||||||||
Cp    977 AGGATCTGGTCACTGGGTTTGCATGCCTTTATTGTTTTT 939
```